

CRF Errors Corrected by the STIC Systems Branch

1600

Serial Number:

09/672,725B

ENTERED

CRF Processing Date:

10/22/2002

Edited by:

Verified by:

(STIC staff)

☐

Changed a file from non-ASCII to ASCII

☐

Changed the margins in cases where the sequence text was "wrapped" down to the next line.

1652

☐

Edited a format error in the Current Application Data section, specifically:

☐

Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_

☐

Added the mandatory heading and subheadings for "Current Application Data".

☐

Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐

Changed the spelling of a mandatory field (the headings or subheadings), specifically:

☐

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

☐

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

☐

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐

Inserted colons after headings/subheadings. Headings edited included:

☐

Deleted extra, invalid, headings used by an applicant, specifically:

☒

Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_

☐

Inserted mandatory headings, specifically: \_\_\_\_\_

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☐

Corrected an obvious error in the response, specifically: \_\_\_\_\_

OCT 25 2002

☐

Edited identifiers where upper case is used but lower case is required, or vice versa

TECH CENTER 1600/2900

☐

Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_

☐

A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐

Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_

☐

Other: \_\_\_\_\_

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



1600

## RAW SEQUENCE LISTING

DATE: 10/22/2002

PATENT APPLICATION: US/09/672,725B

TIME: 19:21:18

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\10222002\I672725B.raw

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OCT 25 2002

TECH CENTER 1600/2900

4 <110> APPLICANT: Stocker, Penny J.  
 5 Steimel-Crespi, Dorothy T.  
 6 Crespi, Charles L.  
 7 Rief, Timothy C  
 8 Patten, Christopher J.

10 <120> TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF  
 13 <130> FILE REFERENCE: G0307/7017  
 15 <140> CURRENT APPLICATION NUMBER: US 09/672,725B  
 16 <141> CURRENT FILING DATE: 2000-09-28  
 18 <150> PRIOR APPLICATION NUMBER: US 60/156,510  
 19 <151> PRIOR FILING DATE: 1999-09-28  
 21 <160> NUMBER OF SEQ ID NOS: 32  
 23 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 4279  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Canis familiaris  
 30 <220> FEATURE:  
 31 <221> NAME/KEY: CDS  
 32 <222> LOCATION: (17)...(3859)  
 34 <400> SEQUENCE: 1

35	ggagcgcgag gtcggg atg gat cct gaa gga ggc cgt aag ggg agt gca gag	52
36	Met Asp Pro Glu Gly Gly Arg Lys Gly Ser Ala Glu	
37	1 5 10	
39	aag aac ttc tgg aaa atg ggc aaa aaa agt aaa aaa aat gag aag aaa	100
40	Lys Asn Phe Trp Lys Met Gly Lys Lys Ser Lys Lys Asn Glu Lys Lys	
41	15 20 25	
43	gaa aag aaa cca act gtc agc acg ttt gca atg ttt cgc tat tca aat	148
44	Glu Lys Lys Pro Thr Val Ser Thr Phe Ala Met Phe Arg Tyr Ser Asn	
45	30 35 40	
47	tgg ctt gat agg ttg tat atg ttg gtg ggg aca atg gct gcc atc atc	196
48	Trp Leu Asp Arg Leu Tyr Met Leu Val Gly Thr Met Ala Ala Ile Ile	
49	45 50 55 60	
51	cat gga gct gca ctc cct ctc atg atg ctg gtt ttt gga aac atg aca	244
52	His Gly Ala Ala Leu Pro Leu Met Met Leu Val Phe Gly Asn Met Thr	
53	65 70 75	
55	gat agc ttt gca aat gca gga att tca aga aac aaa act ttt cca gtt	292
56	Asp Ser Phe Ala Asn Ala Gly Ile Ser Arg Asn Lys Thr Phe Pro Val	
57	80 85 90	
59	ata att aat gaa agt att acg aac aat aca caa cat ttc atc aac cat	340
60	Ile Ile Asn Glu Ser Ile Thr Asn Asn Thr Gln His Phe Ile Asn His	
61	95 100 105	
63	ctg gag gag gaa atg acc acg tat gcc tat tat tac agt ggg atc ggt	388

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64	Leu	Glu	Glu	Glu	Met	Thr	Thr	Tyr	Ala	Tyr	Tyr	Tyr	Ser	Gly	Ile	Gly	
65		110					115				120						
67	gct	ggc	gtg	ctg	gtg	gct	gct	tac	atc	cag	gtt	tca	ttc	tgg	tgc	ctg	436
68	Ala	Gly	Val	Leu	Val	Ala	Ala	Tyr	Ile	Gln	Val	Ser	Phe	Trp	Cys	Leu	
69	125					130					135					140	
71	gca	gca	gga	aga	cag	ata	ctc	aaa	att	aga	aaa	caa	ttt	ttt	cat	gct	484
72	Ala	Ala	Gly	Arg	Gln	Ile	Leu	Lys	Ile	Arg	Lys	Gln	Phe	Phe	His	Ala	
73					145					150						155	
75	atc	atg	cga	cag	gag	att	ggc	tgg	ttt	gac	gtg	cat	gac	gtt	ggg	gag	532
76	Ile	Met	Arg	Gln	Glu	Ile	Gly	Trp	Phe	Asp	Val	His	Asp	Val	Gly	Glu	
77				160					165					170			
79	ctt	aac	acc	cgg	ctc	aca	gac	gat	gtc	tcc	aaa	atc	aat	gaa	gga	att	580
80	Leu	Asn	Thr	Arg	Leu	Thr	Asp	Asp	Val	Ser	Lys	Ile	Asn	Glu	Gly	Ile	
81		175						180					185				
83	ggc	gac	aaa	att	gga	atg	ttc	ttt	cac	tca	ata	gca	aca	ttt	ttc	acc	628
84	Gly	Asp	Lys	Ile	Gly	Met	Phe	Phe	His	Ser	Ile	Ala	Thr	Phe	Phe	Thr	
85		190					195					200					
87	ggt	ttt	ata	gtg	ggg	ttt	aca	cgt	ggt	tgg	aag	cta	acc	ctt	gtg	att	676
88	Gly	Phe	Ile	Val	Gly	Phe	Thr	Arg	Gly	Trp	Lys	Leu	Thr	Leu	Val	Ile	
89	205					210					215					220	
91	ttg	gcc	atc	agc	cct	ggt	ctt	gga	ctt	tca	gcc	gcc	atc	tgg	gca	aag	724
92	Leu	Ala	Ile	Ser	Pro	Val	Leu	Gly	Leu	Ser	Ala	Ala	Ile	Trp	Ala	Lys	
93					225					230					235		
95	ata	cta	tct	tca	ttt	act	gat	aaa	gaa	ctc	ttg	gcc	tat	gca	aaa	gct	772
96	Ile	Leu	Ser	Ser	Phe	Thr	Asp	Lys	Glu	Leu	Leu	Ala	Tyr	Ala	Lys	Ala	
97				240					245					250			
99	gga	gca	gta	gct	gaa	gaa	gtc	tta	gca	gca	atc	aga	act	gtg	att	gcc	820
100	Gly	Ala	Val	Ala	Glu	Glu	Val	Leu	Ala	Ala	Ile	Arg	Thr	Val	Ile	Ala	
101			255					260						265			
103	ttt	gga	gga	caa	aag	aaa	gaa	ctt	gaa	agg	tac	aac	aaa	aat	tta	gaa	868
104	Phe	Gly	Gly	Gln	Lys	Lys	Glu	Leu	Glu	Arg	Tyr	Asn	Lys	Asn	Leu	Glu	
105		270					275					280					
107	gaa	gct	aaa	gga	att	ggg	ata	aag	aaa	gct	atc	acg	gcc	aac	att	tct	916
108	Glu	Ala	Lys	Gly	Ile	Gly	Ile	Lys	Lys	Ala	Ile	Thr	Ala	Asn	Ile	Ser	
109	285					290					295					300	
111	att	ggt	gcc	gct	ttc	tta	ttg	atc	tat	gca	tca	tat	gct	ctg	gct	ttc	964
112	Ile	Gly	Ala	Ala	Phe	Leu	Leu	Ile	Tyr	Ala	Ser	Tyr	Ala	Leu	Ala	Phe	
113					305					310					315		
115	tgg	tat	ggg	acc	tcc	ttg	gtc	ctc	tcc	agt	gaa	tat	tct	att	gga	caa	1012
116	Trp	Tyr	Gly	Thr	Ser	Leu	Val	Leu	Ser	Ser	Glu	Tyr	Ser	Ile	Gly	Gln	
117			320						325					330			
119	gta	ctc	act	gtc	ttc	ttt	tct	gta	tta	att	ggg	gct	ttt	agt	att	gga	1060
120	Val	Leu	Thr	Val	Phe	Phe	Ser	Val	Leu	Ile	Gly	Ala	Phe	Ser	Ile	Gly	
121			335					340					345				
123	cag	gca	tcc	cca	agc	att	gaa	gca	ttt	gca	aac	gca	aga	gga	gca	gct	1108
124	Gln	Ala	Ser	Pro	Ser	Ile	Glu	Ala	Phe	Ala	Asn	Ala	Arg	Gly	Ala	Ala	
125		350					355					360					
127	tat	gaa	atc	ttc	aag	ata	att	gac	aat	aaa	cca	agc	att	gac	agc	tat	1156
128	Tyr	Glu	Ile	Phe	Lys	Ile	Ile	Asp	Asn	Lys	Pro	Ser	Ile	Asp	Ser	Tyr	

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129	365		370		375		380	
131	tcg aag agt gga cat aaa cca gat aat att aag gga aat ttg gaa ttc	1204						
132	Ser Lys Ser Gly His Lys Pro Asp Asn Ile Lys Gly Asn Leu Glu Phe							
133			385		390		395	
135	aaa aat gtt cac ttc agt tac cct tct cga aaa gaa gtt aag atc tta	1252						
136	Lys Asn Val His Phe Ser Tyr Pro Ser Arg Lys Glu Val Lys Ile Leu							
137			400		405		410	
139	aag ggt ctc aac ctg aag gtt cag agt ggg cag aca gtg gcg ctg gtt	1300						
140	Lys Gly Leu Asn Leu Lys Val Gln Ser Gly Gln Thr Val Ala Leu Val							
141			415		420		425	
143	ggg aac agt ggc tgc ggg aag agc acg acc gtg cag ctg atg cag agg	1348						
144	Gly Asn Ser Gly Cys Gly Lys Ser Thr Thr Val Gln Leu Met Gln Arg							
145			430		435		440	
147	ctc tat gac ccc aca gat ggc atg gtc tgt att gat gga cag gac att	1396						
148	Leu Tyr Asp Pro Thr Asp Gly Met Val Cys Ile Asp Gly Gln Asp Ile							
149			445		450		455	
151	agg acc ata aat gta agg cat ctt cgg gaa att act ggt gtg gtg agt	1444						
152	Arg Thr Ile Asn Val Arg His Leu Arg Glu Ile Thr Gly Val Val Ser							
153			465		470		475	
155	cag gag cct gtg ttg ttt gcc acc acg ata gct gaa aac att cgc tat	1492						
156	Gln Glu Pro Val Leu Phe Ala Thr Thr Ile Ala Glu Asn Ile Arg Tyr							
157			480		485		490	
159	ggc cgc gaa aat gtc acc atg gat gag att gag aaa gct gtt aag gaa	1540						
160	Gly Arg Glu Asn Val Thr Met Asp Glu Ile Glu Lys Ala Val Lys Glu							
161			495		500		505	
163	gcc aat gcc tat gat ttt atc atg aaa cta cct aat aaa ttt gac act	1588						
164	Ala Asn Ala Tyr Asp Phe Ile Met Lys Leu Pro Asn Lys Phe Asp Thr							
165			510		515		520	
167	ctg gtt gga gag aga ggg gcc cag ctg agt ggt gga cag aaa cag aga	1636						
168	Leu Val Gly Glu Arg Gly Ala Gln Leu Ser Gly Gly Gln Lys Gln Arg							
169			525		530		535	
171	atc gcc att gct cgg gcc ctg gtt cgc aac ccc aag att ctt ctg ctg	1684						
172	Ile Ala Ile Ala Arg Ala Leu Val Arg Asn Pro Lys Ile Leu Leu Leu							
173			545		550		555	
175	gat gag gca acg tca gct ctg gac act gaa agt gaa gca gtg gtt cag	1732						
176	Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser Glu Ala Val Val Gln							
177			560		565		570	
179	gtg gcc ctg gat aag gcc aga aaa ggc cgg act acc att gtg ata gct	1780						
180	Val Ala Leu Asp Lys Ala Arg Lys Gly Arg Thr Thr Ile Val Ile Ala							
181			575		580		585	
183	cat cgt ttg tct aca gtt cgt aat gcc gat gtc att gct ggt ttt gat	1828						
184	His Arg Leu Ser Thr Val Arg Asn Ala Asp Val Ile Ala Gly Phe Asp							
185			590		595		600	
187	gat gga gtc att gtg gag aaa gga aat cat gat gaa ctc atg aaa gag	1876						
188	Asp Gly Val Ile Val Glu Lys Gly Asn His Asp Glu Leu Met Lys Glu							
189			605		610		615	
191	aag ggc att tac ttc aaa ctt gtc aca atg cag aca aga gga aat gaa	1924						
192	Lys Gly Ile Tyr Phe Lys Leu Val Thr Met Gln Thr Arg Gly Asn Glu							
193			625		630		635	

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195	att gag tta gaa aat gcc act ggt gaa tcc aaa agt gaa agt gat gcc	1972
196	Ile Glu Leu Glu Asn Ala Thr Gly Glu Ser Lys Ser Glu Ser Asp Ala	
197	640 645 650	
199	ttg gaa atg tct cca aaa gat tca ggg tcc agt tta ata aaa aga aga	2020
200	Leu Glu Met Ser Pro Lys Asp Ser Gly Ser Ser Leu Ile Lys Arg Arg	
201	655 660 665	
203	tca act cgc agg agt ata cat gca cca caa ggc caa gac aga aag ctt	2068
204	Ser Thr Arg Arg Ser Ile His Ala Pro Gln Gly Gln Asp Arg Lys Leu	
205	670 675 680	
207	ggt aca aaa gag gac ttg aat gag aat gta cct cca gtt tcc ttc tgg	2116
208	Gly Thr Lys Glu Asp Leu Asn Glu Asn Val Pro Pro Val Ser Phe Trp	
209	685 690 695 700	
211	agg att ctg aag ctg aac tca act gaa tgg cct tat ttt gtg gtt ggt	2164
212	Arg Ile Leu Lys Leu Asn Ser Thr Glu Trp Pro Tyr Phe Val Val Gly	
213	705 710 715	
215	ata ttt tgt gct att ata aac gga ggc ctg caa cca gca ttt tca ata	2212
216	Ile Phe Cys Ala Ile Ile Asn Gly Gly Leu Gln Pro Ala Phe Ser Ile	
217	720 725 730	
219	ata ttt tca agg att ata ggg atc ttt acc cga gat gag gat cct gaa	2260
220	Ile Phe Ser Arg Ile Ile Gly Ile Phe Thr Arg Asp Glu Asp Pro Glu	
221	735 740 745	
223	aca aaa cga cag aat agt aac atg ttt tct gta ttg ttt cta gtc ctt	2308
224	Thr Lys Arg Gln Asn Ser Asn Met Phe Ser Val Leu Phe Leu Val Leu	
225	750 755 760	
227	gga att att tct ttt att aca ttt ttc ctc cag ggc ttc aca ttt ggc	2356
228	Gly Ile Ile Ser Phe Ile Thr Phe Phe Leu Gln Gly Phe Thr Phe Gly	
229	765 770 775 780	
231	aaa gct ggg gag atc ctc act aag cgg ctt cga tac atg gtt ttc aga	2404
232	Lys Ala Gly Glu Ile Leu Thr Lys Arg Leu Arg Tyr Met Val Phe Arg	
233	785 790 795	
235	tcc atg ctg aga cag gat gtc agc tgg ttt gat gac cct aaa aac acc	2452
236	Ser Met Leu Arg Gln Asp Val Ser Trp Phe Asp Asp Pro Lys Asn Thr	
237	800 805 810	
239	act gga gca ttg aca acc agg ctt gcc aat gat gcg gct caa gtt aaa	2500
240	Thr Gly Ala Leu Thr Thr Arg Leu Ala Asn Asp Ala Ala Gln Val Lys	
241	815 820 825	
243	ggg gct ata ggt tcc agg ctt gct gtc att acc cag aat ata gca aat	2548
244	Gly Ala Ile Gly Ser Arg Leu Ala Val Ile Thr Gln Asn Ile Ala Asn	
245	830 835 840	
247	ctt ggg aca ggc att att ata tcc tta atc tat ggt tgg caa tta aca	2596
248	Leu Gly Thr Gly Ile Ile Ile Ser Leu Ile Tyr Gly Trp Gln Leu Thr	
249	845 850 855 860	
251	ctt tta ctc tta gca att gta ccc atc att gca ata gca gga gtt gtt	2644
252	Leu Leu Leu Leu Ala Ile Val Pro Ile Ile Ala Ile Ala Gly Val Val	
253	865 870 875	
255	gaa atg aaa atg ttg tct gga caa gca ctg aaa gat aag aaa gag cta	2692
256	Glu Met Lys Met Leu Ser Gly Gln Ala Leu Lys Asp Lys Lys Glu Leu	
257	880 885 890	
259	gaa gga gct ggg aag att gct aca gaa gcc atc gaa aac ttc cga act	2740

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260	Glu Gly Ala Gly Lys Ile Ala Thr Glu Ala Ile Glu Asn Phe Arg Thr	
261	895 900 905	
263	gtt gtt tct ttg act cgg gag cag aag ttt gaa tac atg tat gca cag	2788
264	Val Val Ser Leu Thr Arg Glu Gln Lys Phe Glu Tyr Met Tyr Ala Gln	
265	910 915 920	
267	agt ttg caa gta cca tac aga aac tct ttg agg aaa gca cac atc ttc	2836
268	Ser Leu Gln Val Pro Tyr Arg Asn Ser Leu Arg Lys Ala His Ile Phe	
269	925 930 935 940	
271	ggg gtc tca ttt tct atc acc cag gca atg atg tat ttt tcc tat gct	2884
272	Gly Val Ser Phe Ser Ile Thr Gln Ala Met Met Tyr Phe Ser Tyr Ala	
273	945 950 955	
275	ggc tgt ttc cgg ttt ggt gcc tac ttg gtg gca aat gag ttc atg aac	2932
276	Gly Cys Phe Arg Phe Gly Ala Tyr Leu Val Ala Asn Glu Phe Met Asn	
277	960 965 970	
279	ttt cag gat gtt ctt ttg gta ttc tca gct att gtc ttt ggt gcc atg	2980
280	Phe Gln Asp Val Leu Leu Val Phe Ser Ala Ile Val Phe Gly Ala Met	
281	975 980 985	
283	gca gtg ggg cag gtc agt tca ttt gct cct gac tat gcc aaa gcc aaa	3028
284	Ala Val Gly Gln Val Ser Ser Phe Ala Pro Asp Tyr Ala Lys Ala Lys	
285	990 995 1000	
287	gta tca gca gcc cac gtc atc atg atc att gaa aaa agc cct ctg att	3076
288	Val Ser Ala Ala His Val Ile Met Ile Ile Glu Lys Ser Pro Leu Ile	
289	1005 1010 1015 1020	
291	gac agc tac agc cct cac ggc ctc aag cca aat acg ttg gaa gga aat	3124
292	Asp Ser Tyr Ser Pro His Gly Leu Lys Pro Asn Thr Leu Glu Gly Asn	
293	1025 1030 1035	
295	gtg aca ttt aat gag gtc gtg ttc aac tat ccc act cga cca gac atc	3172
296	Val Thr Phe Asn Glu Val Val Phe Asn Tyr Pro Thr Arg Pro Asp Ile	
297	1040 1045 1050	
299	ccc gtg ctc cag ggg ctg agc ctc gag gtg aag aag ggc cag acg ctg	3220
300	Pro Val Leu Gln Gly Leu Ser Leu Glu Val Lys Lys Gly Gln Thr Leu	
301	1055 1060 1065	
303	gcc ctc gta ggt agc agt ggc tgt ggg aag agc aca gtt gtt cag ctc	3268
304	Ala Leu Val Gly Ser Ser Gly Cys Gly Lys Ser Thr Val Val Gln Leu	
305	1070 1075 1080	
307	cta gag cgc ttc tat gac ccc ttg gct ggt tca gtg cta att gat ggc	3316
308	Leu Glu Arg Phe Tyr Asp Pro Leu Ala Gly Ser Val Leu Ile Asp Gly	
309	1085 1090 1095 1100	
311	aaa gag ata aag cac ctg aat gtc cag tgg ctc cga gca cac ctg ggc	3364
312	Lys Glu Ile Lys His Leu Asn Val Gln Trp Leu Arg Ala His Leu Gly	
313	1105 1110 1115	
315	atc gtg tct cag gag ccc atc ctg ttt gac tgc agc att gcc gag aac	3412
316	Ile Val Ser Gln Glu Pro Ile Leu Phe Asp Cys Ser Ile Ala Glu Asn	
317	1120 1125 1130	
319	att gcc tat gga gac aac agc cgg gtc gta tca cat gaa gag att atg	3460
320	Ile Ala Tyr Gly Asp Asn Ser Arg Val Val Ser His Glu Glu Ile Met	
321	1135 1140 1145	
323	cag gca gcc aag gag gcc aac ata cac cac ttc atc gag aca ctc cct	3508
324	Gln Ala Ala Lys Glu Ala Asn Ile His His Phe Ile Glu Thr Leu Pro	

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/672,725B

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:28; N Pos. 1,2

15